

GC GCCCGCGGT CCTTCCCGGAGGTTCTTAGGTCCTTCACTTCCTGTTTGCCGGCACTTCAAAATCCGGGTCAAAGGGTG SEQ ID NO:1  
TCGCTTCGGTCTCTTCTCCCCGGCTGATCCCAGCACTCTCCGTGACAGCGCCTCCTGACTCAGCCCAGGACCGGCTTCT  
TCTCACGACCTGCTGGAGACTGGACGCCCCACACCTGACCCGGAACTCGGAGGCGTGCTTCCTCCACCCGCCGGCTAGCA  
GCCCCGGGCCCTGAGCTCCCGCCGACGCCGCTGGGGGGCCCCGACAGGCCCTCGGCGCTGATGCTGAGTGGGATCGAGG  
GCCCCGGGGCGGCGGCGGAGTACGGGCCTCTGGCGCCTTAGGCCAGCCGAGGTGTCGGTTCTTAGGCTCTCCAGGCTCG  
CTAGCTCCCCGCCCGGCTTGGATGGGTCTCCCTGCGCCATAAATGTGGCTGCTGAGGCGGCGGTGGCCGTGGCCCCGTCCG  
CGCTGCTGCTGCGGCGCTCCAAGTTCATCTCCGCCCCGGGGCTCTCTGCCCCACCTCGGGGCTGCCGCCACCCGCTCC

	M	D	K	I	L	E	G	L	V	S	S	SEQ ID NO:2
TTATCCCCTGGCCCTGGCCTTGCAGCGTGGCGACA	ATG	GAC	AAG	ATC	CTG	GAG	GGC	CTT	GTG	AGT	TCC	33
	↑SEQ ID NO:3→											
S H P L P L K R V I V R K V V E S A E H												31
TCG CAT CCC CTG CCC CTC AAG CGG GTG ATT GTG CGG AAG GTG GTG GAA TCG GCG GAG CAC												93
W L D E A Q C E A M F D L T T R L I L E												51
TGG CTA GAC GAG GCG CAG TGC GAG GCC ATG TTT GAC CTG ACG ACC CGG CTC ATC CTG GAG												153
G Q D P F Q R Q V G H Q V L E A Y A R Y												71
GGC CAG GAC CCT TTC CAG CGG CAG GTG GGG CAC CAG GTG CTG GAG GCC TAC GCA CGA TAC												213
H R P E F E S F F N K T F V L G L L H Q												91
CAC CGG CCA GAG TTC GAG TCC TTC TTC AAC AAG ACC TTC GTG TTG GGC CTC CTT CAT CAG												273
G Y H S L D R K D V A I L D Y I H N G L												111
GGC TAC CAC TCT CTG GAC AGG AAG GAT GTA GCC ATC CTG GAC TAC ATT CAC AAC GGC CTG												333
K L I M S C P S V L D L F S L L Q V E V												131
AAG CTG ATT ATG AGC TGT CCG TCG GTG CTG GAT CTC TTT AGC CTC CTG CAG GTA GAG GTG												393
L R M V C E R P E P Q L C A R L S D L L												151
TTA CGG ATG GTG TGT GAG AGG CCG GAG CCG CAG CTC TGT GCC CGA CTG AGC GAC CTT CTG												453
T D F V Q C I P K G K L S I T F C Q Q L												171
ACC GAC TTT GTG CAA TGC ATC CCC AAG GGG AAA TTG TCC ATC ACG TTC TGT CAA CAG CTG												513
V R T I G H F Q C V S T Q E R E L R E Y												191
GTT CGA ACG ATA GGC CAT TTC CAG TGC GTG TCC ACC CAG GAA AGA GAG CTG CAA GAA TAT												573
V S Q V T K V S N L L Q N I W K A E P A												211
GTC TCC CAG GTG ACA AAA GTG AGT AAC TTG CTG CAG AAC ATC TGG AAG GCC GAG CCT GCC												633
T L L P S L Q E V F A S I S S T D S F												231
ACA CTA CTG CCT TCC CTG CAA GAA GTT TTT GCA AGC ATC TCT TCC ACA GAT GAA TCA TTT												693
E P S V A L A S L V Q H I P L Q M I T V												251
GAA CCT TCT GTA GCA TTG GCA AGC CTT GTG CAG CAT ATT CCT CTT CAG ATG ATT ACA GTT												753
L I R S L T T D P N V K D A S M T Q A L												271

FIG 1A

CTC	ATC	AGG	AGC	CTT	ACT	ACG	GAT	CCA	AAT	GTA	AAA	GAT	GCA	AGT	ATG	ACC	CAA	GCC	CTT	813
C	R	M	I	D	W	L	S	W	P	L	A	Q	H	V	D	T	W	V	I	291
TGC	AGA	ATG	ATT	GAC	TGG	CTA	TCC	TGG	CCA	TTG	GCT	CAG	CAT	GTG	GAT	ACA	TGG	GTA	ATT	873
A	L	I	K	G	L	A	A	V	Q	K	F	T	I	L	I	D	V	T	L	311
GCA	CTC	CTG	AAA	GGA	CTG	GCA	GCT	GTC	CAG	AAG	TTT	ACT	ATT	TTG	ATA	GAT	GTT	ACT	TTG	933
L	K	I	E	L	V	F	N	R	L	W	F	P	L	V	R	P	G	A	L	331
CTG	AAA	ATA	GAA	CTG	GTT	TTT	AAT	CGA	CTT	TGG	TTT	CCT	CTT	GTG	AGA	CCT	GGT	GCT	CTT	993
A	V	L	S	H	M	L	L	S	F	Q	H	S	P	E	A	F	H	L	I	351
GCA	GTT	CTT	TCT	CAC	ATG	CTG	CTT	AGC	TTT	CAG	CAT	TCT	CCA	GAG	GCG	TTC	CAT	TTG	ATT	1053
V	P	H	V	V	N	L	V	H	S	F	K	N	D	G	L	P	S	S	T	371
GTT	CCT	CAT	GTG	GTT	AAT	TTG	GTT	CAT	TCT	TTC	AAA	AAT	GAT	GGT	CTG	CCT	TCA	AGT	ACA	1113
A	F	L	V	Q	L	T	E	L	I	H	C	M	M	Y	H	Y	S	G	F	391
GCC	TTC	TTA	GTA	CAA	TTA	ACA	GAA	TTG	ATA	CAC	TGT	ATG	ATG	TAT	CAT	TAT	TCT	GGA	TTT	1173
P	D	L	Y	E	P	I	L	E	A	I	K	D	F	P	K	P	S	E	E	411
CCA	GAT	CTC	TAT	GAA	CCT	ATT	CTG	GAG	GCA	ATA	AAG	GAT	TTT	CCT	AAG	CCC	AGT	GAA	GAG	1233
K	I	K	L	I	L	N	Q	S	A	W	T	S	Q	S	N	S	L	A	S	431
AAG	ATT	AAG	TTA	ATT	CTC	AAT	CAA	AGT	GCC	TGG	ACT	TCT	CAA	TCC	AAT	TCT	TTG	GCG	TCT	1293
C	L	S	R	L	S	G	K	S	E	T	G	K	T	G	L	I	N	L	G	451
TGC	TTG	TCT	AGA	CTT	TCT	GGA	AAA	TCT	GAA	ACT	GGG	AAA	ACT	GGT	CTT	ATT	AAC	CTA	GGA	1353
N	T	C	Y	M	N	S	V	I	Q	A	L	F	M	A	T	D	F	R	R	471
AAT	ACA	TGT	TAT	ATG	AAC	AGT	GTT	ATA	CAA	GCC	TTG	TTT	ATG	GCC	ACA	GAT	TTC	AGG	AGA	1413
Q	V	L	S	L	N	L	N	G	C	N	S	L	M	K	K	L	Q	H	L	491
CAA	GTA	TTA	TCT	TTA	AAT	CTA	AAT	GGG	TGC	AAT	TCA	TTA	ATG	AAA	AAA	TTA	CAG	CAT	CTT	1473
F	A	F	L	A	H	T	Q	R	E	A	Y	A	P	R	I	F	F	E	A	511
TTT	GCC	TTT	CTG	GCC	CAT	ACA	CAG	AGG	GAA	GCA	TAC	GCA	CCT	CGG	ATA	TTC	TTT	GAG	GCT	1533
S	R	P	P	W	F	T	P	R	S	Q	Q	D	C	S	E	Y	L	R	F	531
TCC	AGA	CCT	CCA	TGG	TTT	ACT	CCC	AGA	TCA	CAG	CAA	GAC	TGT	TCT	GAA	TAC	CTC	AGA	TTT	1593
L	L	D	R	L	H	E	E	E	K	I	L	K	V	Q	A	S	H	K	P	551
CTC	CTT	GAC	AGG	CTC	CAT	GAA	GAA	GAA	AAG	ATC	TTG	AAA	GTT	CAG	GCC	TCA	CAC	AAG	CCT	1653
S	E	I	L	E	C	S	E	T	S	L	Q	E	V	A	S	K	A	A	V	571
TCT	GAA	ATT	CTG	CAA	TGC	AGT	GAA	ACT	TCT	TTA	CAG	GAA	GTA	GCT	AGT	AAA	GCA	GCA	GTA	1713
L	T	E	T	P	R	T	S	D	G	E	K	T	L	I	E	K	M	F	G	591
CTA	ACA	GAG	ACC	CCT	CGT	ACA	AGT	GAC	GGT	GAG	AAG	ACT	TTA	ATA	GAA	AAA	ATG	TTT	GGA	1773
G	K	L	R	T	H	I	R	C	L	N	C	R	S	T	S	Q	K	V	E	611
GGA	AAA	CTA	CGA	ACT	CAC	ATA	CGT	TGT	TTG	AAC	TGC	AGG	AGT	ACC	TCA	CAA	AAA	GTG	GAA	1833
A	F	T	D	L	S	L	A	F	C	P	S	S	S	L	E	N	M	S	V	631
GCC	TTT	ACA	GAT	CTT	TCG	CTT	GCC	TTT	TGT	CCT	TCC	TCT	TCT	TTG	GAA	AAC	ATG	TCT	GTC	1893
Q	D	P	A	S	S	P	S	I	Q	D	G	G	L	M	Q	A	S	V	P	651

FIG 1B

CAA	GAT	CCA	GCA	TCA	TCA	CCC	AGT	ATA	CAA	GAT	GGT	GGT	CTA	ATG	CAA	GCC	TCT	GTA	CCC	1953
G	P	S	E	E	P	V	V	Y	N	P	T	T	A	A	F	I	C	D	S	671
GGT	CCT	TCA	GAA	GAA	CCA	GTA	GTT	TAT	AAT	CCA	ACA	ACA	GCT	GCC	TTC	ATC	TGT	GAC	TCA	2013
L	V	N	E	K	T	I	G	S	P	P	N	E	F	Y	C	S	E	N	T	691
CTT	GTG	AAT	GAA	AAA	ACC	ATA	GGC	AGT	CCT	CCT	AAT	GAG	TTT	TAC	TGT	TCT	GAA	AAC	ACT	2073
S	V	P	N	E	S	N	K	I	L	V	N	K	D	V	P	Q	K	P	G	711
TCT	GTC	CCT	AAC	GAA	TCT	AAC	AAG	ATT	CTT	GTT	AAT	AAA	GAT	GTA	CCT	CAG	AAA	CCA	GGA	2133
G	E	T	T	P	S	V	T	D	L	L	N	Y	F	L	A	P	E	I	L	731
GGT	GAA	ACC	ACA	CCT	TCA	GTA	ACT	GAC	TTA	CTA	AAT	TAT	TTT	TTG	GCT	CCA	GAG	ATT	CTT	2193
T	G	D	N	Q	Y	Y	C	E	N	C	A	S	L	Q	N	A	E	K	T	751
ACT	GGT	GAT	AAC	CAA	TAT	TAT	TGT	GAA	AAC	TGT	GCC	TCT	CTG	CAA	AAT	GCT	GAG	AAA	ACT	2253
M	Q	I	T	E	E	P	E	Y	L	I	L	T	L	L	R	F	S	Y	D	771
ATG	CAA	ATC	ACG	GAG	GAA	CCT	GAA	TAC	CTT	ATT	CTT	ACT	CTC	CTG	AGA	TTT	TCA	TAT	GAT	2313
Q	K	Y	H	V	R	R	K	I	L	D	N	V	S	L	P	L	V	L	E	791
CAG	AAG	TAT	CAT	GTG	AGA	AGG	AAA	ATT	TTA	GAC	AAT	GTA	TCA	CTG	CCA	CTG	GTT	TTG	GAG	2373
L	P	V	K	R	I	T	S	F	S	S	L	S	E	S	W	S	V	D	V	811
TTG	CCA	GTT	AAA	AGA	ATT	ACT	TCT	TTC	TCT	TCA	TTG	TCA	GAA	AGT	TGG	TCT	GTA	GAT	GTT	2433
D	F	T	D	L	S	E	N	L	A	K	K	L	K	P	S	G	T	D	E	831
GAC	TTC	ACT	GAT	CTT	AGT	GAG	AAC	CTT	GCT	AAA	AAA	TTA	AAG	CCT	TCA	GGG	ACT	GAT	GAA	2493
A	S	C	T	K	L	V	P	Y	L	L	S	S	V	V	V	H	S	G	I	851
GCT	TCC	TGC	ACA	AAA	TTG	GTG	CCC	TAT	CTA	TTA	AGT	TCC	GTT	GTG	GTT	CAC	TCT	GGT	ATA	2553
S	S	E	S	G	H	Y	Y	S	Y	A	R	N	I	T	S	T	D	S	S	871
TCC	TCT	GAA	AGT	GGG	CAT	TAC	TAT	TCT	TAT	GCC	AGA	AAT	ATC	ACA	AGT	ACA	GAC	TCT	TCA	2613
Y	Q	M	Y	H	Q	S	E	A	L	A	L	A	S	S	Q	S	H	L	L	891
TAT	CAG	ATG	TAC	CAC	CAG	TCT	GAG	GCT	CTG	GCA	TTA	GCA	TCC	TCC	CAG	AGT	CAT	TTA	CTA	2673
G	R	D	S	P	S	A	V	F	E	Q	D	L	E	N	K	E	M	S	K	911
GGG	AGA	GAT	AGT	CCC	AGT	GCA	GTT	TTT	GAA	CAG	GAT	TTG	GAA	AAT	AAG	GAA	ATG	TCA	AAA	2733
E	W	F	L	F	N	D	S	R	V	T	F	T	S	F	Q	S	V	Q	K	931
GAA	TGG	TTT	TTA	TTT	AAT	GAC	AGT	AGA	GTG	ACA	TTT	ACT	TCA	TTT	CAG	TCA	GTC	CAG	AAA	2793
I	T	S	R	F	P	K	D	T	A	Y	V	L	L	Y	K	K	Q	H	S	951
ATT	ACG	AGC	AGG	TTT	CCG	AAG	GAC	ACA	GCT	TAT	GTG	CTT	TTG	TAT	AAA	AAA	CAG	CAT	AGT	2853
T	N	G	L	S	G	N	N	P	T	S	G	L	W	I	N	G	D	P	P	971
ACT	AAT	GGT	TTA	AGT	GGT	AAT	AAC	CCA	ACC	AGT	GGA	CTC	TGG	ATA	AAT	GGA	GAC	CCA	CCT	2913
L	Q	K	E	L	M	D	A	I	T	K	D	N	K	L	Y	L	Q	E	Q	991
CTA	CAG	AAA	GAA	CTT	ATG	GAT	GCT	ATA	ACA	AAA	GAC	AAT	AAA	CTA	TAT	TTA	CAC	GAA	CAA	2973
E	L	N	A	R	A	R	A	L	Q	A	A	S	A	S	C	S	F	R	P	1011
GAG	TTG	AAT	GCT	CGA	GCC	CGG	GCC	CTC	CAA	GCT	GCA	TCT	GCT	TCA	TGT	TCA	TTT	CGG	CCC	3033
N	G	F	D	D	N	D	P	P	G	S	C	G	P	T	G	G	G	G	G	1031

FIG 1C

AAT GGA TTT GAT GAC AAC GAC CCA CCA GGA AGC TGT GGA CCA ACT GGT GGA GGG GGT GGA 3093

G G F N T V G R L V F \* 1043  
GGA GGA TTT AAT ACA GTT GGC AGA CTC GTA TTT TGA 3129  
←SEQ ID NO:3↑

TCCTGAGAGAGTCCAAAATGCACTGGTCACGAAACGTCTAATACTATGACTGTTAAAATGTCAGACTATAACAAATATC

TATCTTTTATTTTTCATTAGACCCTTATACTTCAAGAGAACACACTCAGTGCTTGTTTTATTTTCTTGACACATTTAT

TAACAAAATGCATCATGGAAAAAAATCTACCTCTTAAAATTCCATTTGCTTTTATGGTTAGACATGCTTGACCAAAAA

TGTTTCTAGAGAAAATATGTACCTGGTCCCTAATTAAGCTGCGTTAAATTTGGTAGAAGCATTAAATGGTCTATCTTCA

GTTTTACTGAACAAAAAATGTAATTTATTTAGCATTCTTTATAAAAGAATTGATGCTAGAGGTAAAAAAAATACTTGT

TTTTAAAAAATCCTTTACGTCTTGTTGTAATTACCCCATTTAATTTCAAGTCCTTGAAAATCAACTAGAGATTATAAA

GTCTCTAAAGAAGGCAATAACAAAATTTATCAAGATATAGTACTTTTCAGTTTTTGTGTTAGTGTCTTCAGCATCACTGT

GTCTGTATTTCAAGTACAAATGTTTTTTAAAAGGATTCTTTATACATATGTGCTGAATTGATTTTAAGGAAAGTTGCAT

GATCCTGTAGGAGCAACATTTTACCTAAAAAATGCTAACTTTATAGTATTTCTAATTGTTCAAGGATTTTAAAATTCT

GATCCTGTAGGAGCAACATTTTACCTAAAAAATGCTAACTTTATAGTATTTCTAATTGTTCAAGGATTTTAAAATTCT

FIG 1D

Figure 2 shows the results of the analysis of the data from the 1000 ft. well.

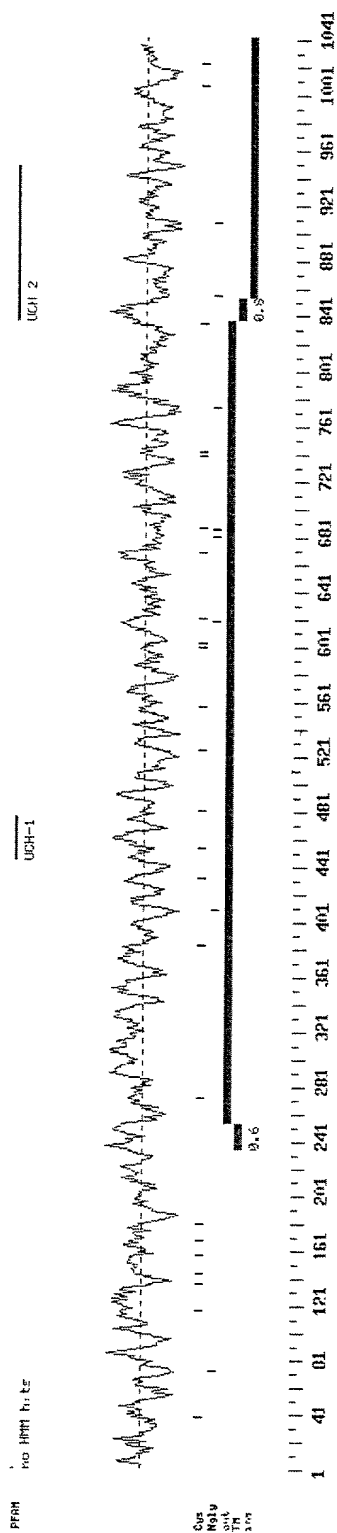


Fig. 2

```

                *->tGLiNlGNTCYmNSvLQcLfsipplrddyldi<-*   SEQ ID NO:4
                tGLiNlGNTCYmNSv+Q+Lf++ ++r+ +l++
23430   445   TGLiNlGNTCYmNSVIQALFMATDFRRQVLSL   476

```

Fig. 3

```

                *->gpqkYeLyaVvvHsGsslsGgHYtayvkken.....   SEQ ID NO:5
                + + Y L +VvvHsG s+ +GHY++y+++ +++++ + +++++
23430   836   KLVPYLLSSVVVHSGISSESCHYYSYARNITstdssyqmyhqseala 882

                .....WykFDDdkVsrvtееevlke
                +++++ +++++ + + + + + + +W++F+D++V+ + v+k
23430   883   lassqshllgrdpsavfeqdlenkemskeWFLFNDSRVFTSFQSVQKI 932

                sggesgdtssAYiLfYer<-*
                + ++AY+L+Y++
23430   933   TSR--FPKDTAYVLLYKK   948

```

Fig. 4

```

Query:   710 PGGETTPSVTDLLNYFLAPEILTGDNQYYCENCASLQNAEKTMQITEPEYLILTLRFS 769 SEQ ID
NO:6

        P G+ + S+ D L F PE L GDN+Y+CE C Q+A K + I + P+ L + L RF
Sbjct:   12 PEGDHS-SLEDCLEQFFKPEELEGDNKHCEKCKKKQDATKQLTIKKLPQVLTiHLKRFE 70

```

Fig. 5